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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/735,995

DATE: 04/03/2001  
TIME: 12:35:42

# 2.

Input Set : N:\Crf3\RULE60\09735995.txt  
Output Set: N:\CRF3\04032001\I735995.raw

ENTERED

5 <110> APPLICANT: Keating, Mark T.  
7 Splawski, Igor  
11 <120> TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT  
13 SYNDROME GENE  
17 <130> FILE REFERENCE: 2323-136  
21 <140> CURRENT APPLICATION NUMBER: 09/735,995  
23 <141> CURRENT FILING DATE: 2000-12-14  
27 <150> PRIOR APPLICATION NUMBER: 09/226,012  
28 <151> PRIOR FILING DATE: 1999-01-06  
31 <160> NUMBER OF SEQ ID NOS: 116  
35 <170> SOFTWARE: PatentIn Ver. 2.0  
39 <210> SEQ ID NO: 1  
41 <211> LENGTH: 3480  
43 <212> TYPE: DNA  
45 <213> ORGANISM: Homo sapiens  
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53 <222> LOCATION: (1)..(3477)  
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61 Met Pro Val Arg Arg Gly His Val Ala Pro Gln Asn Thr Phe Leu Asp  
63 1 5 10 15  
67 acc atc atc cgc aag ttt gag ggc cag agc cgt aag ttc atc atc gcc 96  
69 Thr Ile Ile Arg Lys Phe Glu Gly Gln Ser Arg Lys Phe Ile Ile Ala  
71 20 25 30  
75 aac gct cgg gtg gag aac tgc gcc gtc atc tac tgc aac gac ggc ttc 144  
77 Asn Ala Arg Val Glu Asn Cys Ala Val Ile Tyr Cys Asn Asp Gly Phe  
79 35 40 45  
83 tgc gag ctg tgc ggc tac tcg cgg gcc gag gtg atg cag cga ccc tgc 192  
85 Cys Glu Leu Cys Gly Tyr Ser Arg Ala Glu Val Met Gln Arg Pro Cys  
87 50 55 60  
91 acc tgc gac ttc ctg cac ggg ccg cgc acg cag cgc cgc gct gcc gcg 240  
93 Thr Cys Asp Phe Leu His Gly Pro Arg Thr Gln Arg Arg Ala Ala Ala  
95 65 70 75 80  
99 cag atc gcg cag gca ctg ctg ggc gcc gag gag cgc aaa gtg gaa atc 288  
101 Gln Ile Ala Gln Ala Leu Leu Gly Ala Glu Glu Arg Lys Val Glu Ile  
103 85 90 95  
107 gcc ttc tac cgg aaa gat ggg agc tgc ttc cta tgt ctg gtg gat gtg 336  
109 Ala Phe Tyr Arg Lys Asp Gly Ser Cys Phe Leu Cys Leu Val Asp Val  
111 100 105 110  
115 gtg ccc gtg aag aac gag gat ggg gct gtc atc atg ttc atc ctc aat 384  
117 Val Pro Val Lys Asn Glu Asp Gly Ala Val Ile Met Phe Ile Leu Asn  
119 115 120 125  
123 ttc gag gtg gtg atg gag aag gac atg gtg ggg tcc ccg gct cat gac 432  
125 Phe Glu Val Val Met Glu Lys Asp Met Val Gly Ser Pro Ala His Asp  
127 130 135 140  
131 acc aac cac cgg ggc ccc ccc acc agc tgg ctg gcc cca ggc cgc gcc 480

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133	Thr	Asn	His	Arg	Gly	Pro	Pro	Thr	Ser	Trp	Leu	Ala	Pro	Gly	Arg	Ala	
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139	aag	acc	ttc	cgc	ctg	aag	ctg	ccc	gcg	ctg	ctg	gcg	ctg	acg	gcc	cgg	528
141	Lys	Thr	Phe	Arg	Leu	Lys	Leu	Pro	Ala	Leu	Leu	Ala	Leu	Thr	Ala	Arg	
143						165					170					175	
147	gag	tcg	tcg	gtg	cgg	tcg	ggc	ggc	gcg	ggc	ggc	gcg	ggc	gcc	ccg	ggg	576
149	Glu	Ser	Ser	Val	Arg	Ser	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Ala	Pro	Gly	
151						180					185				190		
155	gcc	gtg	gtg	gtg	gac	gtg	gac	ctg	acg	ccc	gcg	gca	ccc	agc	agc	gag	624
157	Ala	Val	Val	Val	Asp	Val	Asp	Leu	Thr	Pro	Ala	Ala	Pro	Ser	Ser	Glu	
159						195					200				205		
163	tcg	ctg	gcc	ctg	gac	gaa	gtg	aca	gcc	atg	gac	aac	cac	gtg	gca	ggg	672
165	Ser	Leu	Ala	Leu	Asp	Glu	Val	Thr	Ala	Met	Asp	Asn	His	Val	Ala	Gly	
167											215				220		
171	ctc	ggg	ccc	gcg	gag	gag	cgg	cgt	gcg	ctg	gtg	ggt	ccc	ggc	tct	cgg	720
173	Leu	Gly	Pro	Ala	Glu	Glu	Arg	Arg	Ala	Leu	Val	Gly	Pro	Gly	Ser	Pro	
175	225					230					235					240	
179	ccc	cgc	agc	gcg	ccc	ggc	cag	ctc	cca	tcg	ccc	cgg	gcg	cac	agc	ctc	768
181	Pro	Arg	Ser	Ala	Pro	Gly	Gln	Leu	Pro	Ser	Pro	Arg	Ala	His	Ser	Leu	
183						245					250				255		
187	aac	ccc	gac	gcc	tcg	ggc	tcc	agc	tgc	agc	ctg	gcc	cgg	acg	cgc	tcc	816
189	Asn	Pro	Asp	Ala	Ser	Gly	Ser	Ser	Cys	Ser	Leu	Ala	Arg	Thr	Arg	Ser	
191						260					265				270		
195	cga	gaa	agc	tgc	gcc	agc	gtg	cgc	cgc	gcc	tcg	tcg	gcc	gac	gac	atc	864
197	Arg	Glu	Ser	Cys	Ala	Ser	Val	Arg	Arg	Ala	Ser	Ser	Ala	Asp	Asp	Ile	
199						275					280				285		
203	gag	gcc	atg	cgc	gcc	ggg	gtg	ctg	ccc	ccg	cca	ccg	cgc	cac	gcc	agc	912
205	Glu	Ala	Met	Arg	Ala	Gly	Val	Leu	Pro	Pro	Pro	Pro	Arg	His	Ala	Ser	
207						295					300						
211	acc	ggg	gcc	atg	cac	cca	ctg	cgc	agc	ggc	ttg	ctc	aac	tcc	acc	tcg	960
213	Thr	Gly	Ala	Met	His	Pro	Leu	Arg	Ser	Gly	Leu	Leu	Asn	Ser	Thr	Ser	
215	305					310					315					320	
219	gac	tcc	gac	ctc	gtg	cgc	tac	cgc	acc	att	agc	aag	att	ccc	caa	atc	1008
221	Asp	Ser	Asp	Leu	Val	Arg	Tyr	Arg	Thr	Ile	Ser	Lys	Ile	Pro	Gln	Ile	
223						325					330				335		
227	acc	ctc	aac	ttt	gtg	gac	ctc	aag	ggc	gac	ccc	ttc	ttg	gct	tcg	ccc	1056
229	Thr	Leu	Asn	Phe	Val	Asp	Leu	Lys	Gly	Asp	Pro	Phe	Leu	Ala	Ser	Pro	
231						340					345				350		
235	acc	agt	gac	cgt	gag	atc	ata	gca	cct	aag	ata	aag	gag	cga	acc	cac	1104
237	Thr	Ser	Asp	Arg	Glu	Ile	Ile	Ala	Pro	Lys	Ile	Lys	Glu	Arg	Thr	His	
239						355					360				365		
243	aat	gtc	act	gag	aag	gtc	acc	cag	gtc	ctg	tcc	ctg	ggc	gcc	gac	gtg	1152
245	Asn	Val	Thr	Glu	Lys	Val	Thr	Gln	Val	Leu	Ser	Leu	Gly	Ala	Asp	Val	
247						375					380						
251	ctg	cct	gag	tac	aag	ctg	cag	gca	ccg	cgc	atc	cac	cgc	tgg	acc	atc	1200
253	Leu	Pro	Glu	Tyr	Lys	Leu	Gln	Ala	Pro	Arg	Ile	His	Arg	Trp	Thr	Ile	
255	385					390					395				400		
259	ctg	cat	tac	agc	ccc	ttc	aag	gcc	gtg	tgg	gac	tgg	ctc	atc	ctg	ctg	1248
261	Leu	His	Tyr	Ser	Pro	Phe	Lys	Ala	Val	Trp	Asp	Trp	Leu	Ile	Leu	Leu	

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263		405		410		415		1296
267	ctg gtc atc tac acg gct gtc ttc aca ccc tac tcg gct gcc ttc ctg							
269	Leu Val Ile Tyr Thr Ala Val Phe Thr Pro Tyr Ser Ala Ala Phe Leu							
271		420		425		430		1344
275	ctg aag gag acg gaa gaa ggc ccg cct gct acc gag tgt ggc tac gcc							
277	Leu Lys Glu Thr Glu Glu Gly Pro Pro Ala Thr Glu Cys Gly Tyr Ala							
279		435		440		445		1392
283	tgc cag ccg ctg gct gtg gtg gac ctc atc gtg gac atc atg ttc att							
285	Cys Gln Pro Leu Ala Val Val Asp Leu Ile Val Asp Ile Met Phe Ile							
287		450		455		460		1440
291	gtg gac atc ctc atc aac ttc cgc acc acc tac gtc aat gcc aac gag							
293	Val Asp Ile Leu Ile Asn Phe Arg Thr Thr Tyr Val Asn Ala Asn Glu							
295	465		470		475		480	1488
299	gag gtg gtc agc cac ccc ggc cgc atc gcc gtc cac tac ttc aag ggc							
301	Glu Val Val Ser His Pro Gly Arg Ile Ala Val His Tyr Phe Lys Gly							
303		485		490		495		1536
307	tgg ttc ctc atc gac atg gtg gcc gcc atc ccc ttc gac ctg ctc atc							
309	Trp Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu Leu Ile							
311		500		505		510		1584
315	ttc ggc tct ggc tct gag gag ctg atc ggg ctg ctg aag act gcg cgg							
317	Phe Gly Ser Gly Ser Glu Glu Leu Ile Gly Leu Leu Lys Thr Ala Arg							
319		515		520		525		1632
323	ctg ctg cgg ctg gtg cgc gtg gcg cgg aag ctg gat cgc tac tca gag							
325	Leu Leu Arg Leu Val Arg Val Ala Arg Lys Leu Asp Arg Tyr Ser Glu							
327		530		535		540		1680
331	tac ggc gcg gcc gtg ctg ttc ttg ctc atg tgc acc ttt gcg ctc atc							
333	Tyr Gly Ala Ala Val Leu Phe Leu Leu Met Cys Thr Phe Ala Leu Ile							
335	545		550		555		560	1728
339	gcg cac tgg cta gcc tgc atc tgg tac gcc atc ggc aac atg gag cag							
341	Ala His Trp Leu Ala Cys Ile Trp Tyr Ala Ile Gly Asn Met Glu Gln							
343		565		570		575		1776
347	cca cac atg gac tca cgc atc ggc tgg ctg cac aac ctg ggc gac cag							
349	Pro His Met Asp Ser Arg Ile Gly Trp Leu His Asn Leu Gly Asp Gln							
351		580		585		590		1824
355	ata ggc aaa ccc tac aac agc agc ggc ctg ggc ggc ccc tcc atc aag							
357	Ile Gly Lys Pro Tyr Asn Ser Ser Gly Leu Gly Gly Pro Ser Ile Lys							
359		595		600		605		1872
363	gac aag tat gtg acg gcg ctc tac ttc acc ttc agc agc ctc acc agt							
365	Asp Lys Tyr Val Thr Ala Leu Tyr Phe Thr Phe Ser Ser Leu Thr Ser							
367		610		615		620		1920
371	gtg ggc ttc ggc aac gtc tct ccc aac acc aac tca gag aag atc ttc							
373	Val Gly Phe Gly Asn Val Ser Pro Asn Thr Asn Ser Glu Lys Ile Phe							
375	625		630		635		640	1968
379	tcc atc tgc gtc atg ctc att ggc tcc ctc atg tat gct agc atc ttc							
381	Ser Ile Cys Val Met Leu Ile Gly Ser Leu Met Tyr Ala Ser Ile Phe							
383		645		650		655		2016
387	ggc aac gtg tcg gcc atc atc cag cgg ctg tac tcg ggc aca gcc cgc							
389	Gly Asn Val Ser Ala Ile Ile Gln Arg Leu Tyr Ser Gly Thr Ala Arg							
391		660		665		670		

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395 tac cac aca cag atg ctg cgg gtg cgg gag ttc atc cgc ttc cac cag 2064  
397 Tyr His Thr Gln Met Leu Arg Val Arg Glu Phe Ile Arg Phe His Gln  
399 675 680 685  
403 atc ccc aat ccc ctg cgc cag cgc ctc gag gag tac ttc cag cac gcc 2112  
405 Ile Pro Asn Pro Leu Arg Gln Arg Leu Glu Glu Tyr Phe Gln His Ala  
407 690 695 700  
411 tgg tcc tac acc aac ggc atc gac atg aac gcg gtg ctg aag ggc ttc 2160  
413 Trp Ser Tyr Thr Asn Gly Ile Asp Met Asn Ala Val Leu Lys Gly Phe  
415 705 710 715 720  
419 cct gag tgc ctg cag gct gac atc tgc ctg cac ctg aac cgc tca ctg 2208  
421 Pro Glu Cys Leu Gln Ala Asp Ile Cys Leu His Leu Asn Arg Ser Leu  
423 725 730 735  
427 ctg cag cac tgc aaa ccc ttc cga ggg gcc acc aag ggc tgc ctt cgg 2256  
429 Leu Gln His Cys Lys Pro Phe Arg Gly Ala Thr Lys Gly Cys Leu Arg  
431 740 745 750  
435 gcc ctg gcc atg aag ttc aag acc aca cat gca ccg cca ggg gac aca 2304  
437 Ala Leu Ala Met Lys Phe Lys Thr Thr His Ala Pro Pro Gly Asp Thr  
439 755 760 765  
443 ctg gtg cat gct ggg gac ctg ctc acc gcc ctg tac ttc atc tcc cgg 2352  
445 Leu Val His Ala Gly Asp Leu Leu Thr Ala Leu Tyr Phe Ile Ser Arg  
447 770 775 780  
451 ggc tcc atc gag atc ctg cgg ggc gac gtc gtc gtg gcc atc ctg ggg 2400  
453 Gly Ser Ile Glu Ile Leu Arg Gly Asp Val Val Val Ala Ile Leu Gly  
455 785 790 795 800  
459 aag aat gac atc ttt ggg gag cct ctg aac ctg tat gca agg cct ggc 2448  
461 Lys Asn Asp Ile Phe Gly Glu Pro Leu Asn Leu Tyr Ala Arg Pro Gly  
463 805 810 815  
467 aag tcg aac ggg gat gtg cgg gcc ctc acc tac tgt gac cta cac aag 2496  
469 Lys Ser Asn Gly Asp Val Arg Ala Leu Thr Tyr Cys Asp Leu His Lys  
471 820 825 830  
475 atc cat cgg gac gac ctg ctg gag gtg ctg gac atg tac cct gag ttc 2544  
477 Ile His Arg Asp Asp Leu Leu Glu Val Leu Asp Met Tyr Pro Glu Phe  
479 835 840 845  
483 tcc gac cac ttc tgg tcc agc ctg gag atc acc ttc aac ctg cga gat 2592  
485 Ser Asp His Phe Trp Ser Ser Leu Glu Ile Thr Phe Asn Leu Arg Asp  
487 850 855 860  
491 acc aac atg atc ccg ggc tcc ccc ggc agt acg gag tta gag ggt ggc 2640  
493 Thr Asn Met Ile Pro Gly Ser Pro Gly Ser Thr Glu Leu Glu Gly Gly  
495 865 870 875 880  
499 ttc agt cgg caa cgc aag cgc aag ttg tcc ttc cgc agg cgc acg gac 2688  
501 Phe Ser Arg Gln Arg Lys Arg Lys Leu Ser Phe Arg Arg Arg Thr Asp  
503 885 890 895  
507 aag gac acg gag cag cca ggg gag gtg tcg gcc ttg ggg ccg ggc cgg 2736  
509 Lys Asp Thr Glu Gln Pro Gly Glu Val Ser Ala Leu Gly Pro Gly Arg  
511 900 905 910  
515 gcg ggg gca ggg ccg agt agc cgg ggc cgg ccg ggg ggg ccg tgg ggg 2784  
517 Ala Gly Ala Gly Pro Ser Ser Arg Gly Arg Pro Gly Gly Pro Trp Gly  
519 915 920 925  
523 gag agc ccg tcc agt ggc ccc tcc agc cct gag agc agt gag gat gag 2832

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525 Glu Ser Pro Ser Ser Gly Pro Ser Ser Pro Glu Ser Ser Glu Asp Glu
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533 Gly Pro Gly Arg Ser Ser Ser Pro Leu Arg Leu Val Pro Phe Ser Ser
535 945      950      955      960      2928
539 ccc agg ccc ccc gga gag ccg ccg ggt ggg gag ccc ctg atg gag gac
541 Pro Arg Pro Pro Gly Glu Pro Pro Gly Gly Glu Pro Leu Met Glu Asp
543      965      970      975      2976
547 tgc gag aag agc agc gac act tgc aac ccc ctg tca ggc gcc ttc tca
549 Cys Glu Lys Ser Ser Asp Thr Cys Asn Pro Leu Ser Gly Ala Phe Ser
551      980      985      990      3024
555 gga gtg tcc aac att ttc agc ttc tgg ggg gac agt cgg ggc cgc cag
557 Gly Val Ser Asn Ile Phe Ser Phe Trp Gly Asp Ser Arg Gly Arg Gln
559      995      1000      1005      3072
563 tac cag gag ctc cct cga tgc ccc gcc ccc acc ccc agc ctc ctc aac
565 Tyr Gln Glu Leu Pro Arg Cys Pro Ala Pro Thr Pro Ser Leu Leu Asn
567      1010      1015      1020      3120
571 atc ccc ctc tcc agc ccg ggt ccg ccg ccc ccg ggc gac gtg gag agc
573 Ile Pro Leu Ser Ser Pro Gly Arg Arg Pro Arg Gly Asp Val Glu Ser
575 1025      1030      1035      1040      3168
579 agg ctg gat gcc ctc cag cgc cag ctc aac agg ctg gag acc cgg ctg
581 Arg Leu Asp Ala Leu Gln Arg Gln Leu Asn Arg Leu Glu Thr Arg Leu
583      1045      1050      1055      3216
587 agt gca gac atg gcc act gtc ctg cag ctg cta cag agg cag atg acg
589 Ser Ala Asp Met Ala Thr Val Leu Gln Leu Leu Gln Arg Gln Met Thr
591      1060      1065      1070      3264
595 ctg gtc ccg ccc gcc tac agt gct gtg acc acc ccg ggg cct ggc ccc
597 Leu Val Pro Pro Ala Tyr Ser Ala Val Thr Thr Pro Gly Pro Gly Pro
599      1075      1080      1085      3312
603 act tcc aca tcc ccg ctg ttg ccc gtc agc ccc ctc ccc acc ctc acc
605 Thr Ser Thr Ser Pro Leu Leu Pro Val Ser Pro Leu Pro Thr Leu Thr
607      1090      1095      1100      3360
611 ttg gac tcg ctt tct cag gtt tcc cag ttc atg gcg tgt gag gag ctg
613 Leu Asp Ser Leu Ser Gln Val Ser Gln Phe Met Ala Cys Glu Glu Leu
615 1105      1110      1115      1120      3408
619 ccc ccg ggg gcc cca gag ctt ccc caa gaa ggc ccc aca cga cgc ctc
621 Pro Pro Gly Ala Pro Glu Leu Pro Gln Glu Gly Pro Thr Arg Arg Leu
623      1125      1130      1135      3456
627 tcc cta ccg ggc cag ctg ggg gcc ctc acc tcc cag ccc ctg cac aga
629 Ser Leu Pro Gly Gln Leu Gly Ala Leu Thr Ser Gln Pro Leu His Arg
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637 His Gly Ser Asp Pro Gly Ser
639      1155
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647 <211> LENGTH: 1159
649 <212> TYPE: PRT
651 <213> ORGANISM: Homo sapiens
655 <400> SEQUENCE: 2

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VERIFICATION SUMMARY  
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